



#9

SEQUENCE LISTING

<110> Barber, Elizabeth K

<120> Gene Expression Control Element DNA

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<140> US 09/966,264

<141> 2001-09-28

<150> US 60/237,079

<151> 2000-09-30

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<170> PatentIn version 3.1

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Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys
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taa gta atc aat caa tca ctc ata gcc aag gtg gaa aag atg tat ccc 96
Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro
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atc atg gaa tat tcc tgt tct gat aga aat ctt gtg ctt atc tat gga 144
Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly
35 40 45

att ctt ttg ata tat att tac att ggg aac ctg aat gta gct tga cat 192

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Phe	Ser	Met		Thr	Pro	Val	Ala		Ser	Asn	Ile	Lys	Leu	Ile	Leu
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aca	aac	aac	gtg	taa	tgg	ctt	cat	taa	taa	ggc	ttt	gct	tct	tcc	tgg 288
Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp
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Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu
	90					95					100				
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Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys
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gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt 432
Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe
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ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg 480
Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met
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Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr
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Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe
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aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gta	gtg	gta	tta	tac	tgt 672
Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys
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Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln
				215					220					225	
gtt	tta	cac	gtc	tat	gca	att	gta	caa	aaa	agt	tat	aag	aaa	act	aca 768
Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr
				230					235					240	
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Cys	Lys	Ile	Leu	Ile	Ala	Lys		Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr
			245						250					255	
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His	Phe	Gly	Leu	Phe	Lys	Asn	Leu		Gln	Leu		Arg	Lys	Asn	Tyr

260 265 270
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 Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr
 275 280
 cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga 960
 Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg
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Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys	35	40	45
Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln	50	55	60
Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe	65	70	75
Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg	85	90	95
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Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	
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Arg	Ser	Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His	
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Lys	Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	
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Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu	Met	
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Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr	Leu	Ser	
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Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	
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Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu	Gly	Ala	Glu	Lys	Met	
			165						170					175		
Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	
		180						185					190			
Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu	
		195					200					205				
Arg	Arg	Val	Val	Val	Leu	Tyr	Cys	Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	
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Leu	Leu	Phe	Cys	Lys	Gln	Trp	Gln	Val	Leu	His	Val	Tyr	Ala	Ile	Val	
225					230					235					240	
Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	
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Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	
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Lys	Gln	Leu	Lys	Arg	Lys	Asn	Tyr	Lys	Gly	Lys	Arg	Lys	Lys	Arg	Asn	
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Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn
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Cys Lys Leu Ile

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att att att ttc aac cca agt aaa agc aga gag aaa ata gcc acc tcc 96
 Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser
 20 25 30

acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144
 Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys
 35 40 45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192
 Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly
 50 55 60

tgg gtg ctg gtg atg gta gtg gta gtt gtg aag gtg gtg atg 234
 Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met
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Arg Asn Gly Gln Val Val Lys Leu
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Gly Arg Asn Ser Met Arg Ser Arg Val
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Cys Phe Pro Gly His Asn Val Gly Ser Leu Phe His Met Ala Asp
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Asp Leu Gly Arg Ala Met Glu Ser Leu Val Ser Val Met Thr Asp
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Glu Glu Gly Ala Glu
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Glu Phe Thr Arg Asn Lys Ser Ile Phe Leu
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Arg Val Val Val Leu Tyr Cys Arg Phe Gln
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 Phe Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala
 -60 -55 -50

acc tcc acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg -96
 Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu
 -45 -40 -35

aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc -48
 Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr
 -30 -25 -20

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 Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met Asp Gly
 -15 -10 -5

gtg gtt tga ttg ata gta aaa aaa atg ttc gtt aat aca agt aga gag 48

Val	Val		Leu	Ile	Val	Lys	Lys	Met	Phe	Val	Asn	Thr	Ser	Arg	Glu	
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taa	gta	atc	aat	caa	tca	ctc	ata	gcc	aag	gtg	gaa	aag	atg	tat	ccc	96
	Val	Ile	Asn	Gln	Ser	Leu	Ile	Ala	Lys	Val	Glu	Lys	Met	Tyr	Pro	
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atc	atg	gaa	tat	tcc	tgt	tct	gat	aga	aat	ctt	gtg	ctt	atc	tat	gga	144
Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly	
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Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu	Asn	Val	Ala		His	
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Phe	Ser	Met		Thr	Pro	Val	Ala		Ser	Asn	Ile	Lys	Leu	Ile	Leu	
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aca	aac	aac	gtg	taa	tgg	ctt	cat	taa	taa	ggc	ttt	gct	tct	tcc	tgg	288
Thr	Asn	Asn	Val		Trp	Leu	His			Gly	Phe	Ala	Ser	Ser	Trp	
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Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	
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ctg	tgt	tgt	ctt	cac	cca	gaa	atg	ggg	aat	gat	ttc	cca	aat	ggc	aaa	384
Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	
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gaa	aca	gag	tga	tgc	tat	cta	tct	gca	cct	ttt	gta	aag	tct	gtc	ttt	432
Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	
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ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg	480
Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met	
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gca	gat	gat	ttg	ggc	aga	gcg	atg	gag	tcc	tta	gta	tca	gtc	atg	aca	528
Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr	
			155					160					165			
gat	gaa	gaa	gga	gca	gaa	taa	atg	ttt	tac	aac	tcc	tga	ttc	ccg	cat	576
Asp	Glu	Glu	Gly	Ala	Glu		Met	Phe	Tyr	Asn	Ser		Phe	Pro	His	
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ggg	ttt	tat	aat	att	cat	aca	aca	aag	agg	att	aga	cag	taa	gag	ttt	624
Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe	
			185					190						195		
aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gta	gtg	gta	tta	tac	tgt	672
Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys	
			200					205						210		
aga	ttt	cag	tag	ttt	cta	agt	ctg	tta	ttg	ttt	tgt	taa	caa	tgg	cag	720
Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln	

215	220	225	
gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768		
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr			
230	235	240	
tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg	816		
Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr			
245	250	255	
cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat	864		
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr			
260	265	270	
aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act	912		
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr			
275	280		
cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga	960		
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg			
285	290	295	
aat agc atg aga agc cgt gtt tga tgt taa tta att	996		
Asn Ser Met Arg Ser Arg Val Cys Leu Ile			
300	305		

<210> 52
 <211> 47
 <212> PRT
 <213> human

<400> 52

Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe	
1 5 10 15	
Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala	
20 25 30	
Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala	
35 40 45	

Leu Lys

<210> 53
 <211> 32
 <212> PRT
 <213> human

<400> 53

Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp	
1 5 10 15	
Gly Trp Val Leu Val Met Val Val Val Val Lys Val Val Met	

Val Val

<210> 54
 <211> 1044
 <212> DNA
 <213> mouse

<400> 54

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ccaacaaagt gtgaaagggtg tgtgccatta cacatctttc tcgggtgataa 200
gagccttgct tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250
ttacatttct ccccatcaaa tgacaccatg ctgatccagt attaagctaa 300
tactaacacc atgcaatgct tcattaacaa ggatttgctt cttgctagaa 350
atgggtaaaa acggactgtg gtctgtatac cttcaatgca gcttatgtgt 400
tgtcttttcc tgaaatggta atgactccca atagtggcaa ccaggggtac 450
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tatggaacgc attttgggtt gtttaaaaaa ttataacagt tataaagaaa 900
gattgtaaac taaagtgtgc tttataaaaa aagttgttta taaaaacccc 950
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<210> 55
 <211> 1236

<212> DNA
<213> human

<400> 55

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agttggtgtg gcggtgatgg tggcagtgat aatggtgacc gatggttggg 200
tgctggtgat ggtagtggta gttgtga.ag gtggtgatgg tggtttgatt 250
gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc 300
aatcactcat agccaagggtg gaaaagatgt atcccatcat ggaatattcc 350
tgtttctgata gaaatcttgt gcttatctat ggaattcttt tgatatatat 400
ttacattggg aacctgaatg tagcttgaca tttttccatg taaacaccag 450
tagcctgata caacattaag ctgatactaa caaacaacgt gtaatggctt 500
cattaataag gctttgcttc ttcctggaaa ctggtgaaaa atcaaactt 550
gttgtgtaca ccctcgatgc agcttctgtg ttgtcttcac ccagaaatgg 600
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tcttgattcc cgcattggtt ttataatatt catacaacaa agaggattag 850
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<210> 56
<211> 303

<212> PRT
<213> human

<400> 56

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Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25					30
Asn	Val	Ala	Arg	His	Phe	Ser	Met	Lys	Thr	Pro	Val	Ala	Arg	Ser
				35					40					45
Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His	Lys
				50					55					60
Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu
				65					70					75
Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu
				80					85					90
Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr
				95					100					105
Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	Leu	Ser	Leu	Cys	Phe
				110					115					120
Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu
				125					130					135
Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu
				140					145					150
Gly	Ala	Glu	Lys	Met	Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe
				155					160					165
Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr
				170					175					180
Arg	Asn	Lys	Ser	Ile	Phe	Leu	Arg	Arg	Val	Val	Val	Leu	Tyr	Cys
				185					190					195
Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys	Lys	Gln	Trp
				200					205					210
Gln	Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys
				215					220					225
Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	Leu	Ala	Ile	Ser	Leu
				230					235					240
Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	Lys	Gln	Leu	Lys
				245					250					255
Arg	Lys	Asn	Tyr	Lys	Gly	Lys	Arg	Lys	Lys	Arg	Asn	Gly	Gln	Val

	260		265		270
Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro					
	275		280		285
Lys Pro Lys Arg Gly arg Asn Ser Met Arg Ser Arg Val Arg Cys					
	290		295		300

Lys Leu Ile

<210> 57
 <211> 111
 <212> DNA
 <213> human

<400> 57
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<210> 58
 <211> 260
 <212> DNA
 <213> human

<400> 58
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 ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTTT CCTTCATAAT 200
 TAACAGTTAT AAAGAAAGAA TTATAAAGGA AAAAGAAAAT AACGCAATGG 250
 ACAAGTGGTG 260

<210> 59
 <211> 17
 <212> DNA
 <213> human

<400> 59

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17

<210> 60
 <211> 17
 <212> DNA

<213> human

<400> 60

gcggtgatgg tggcagt

17

<210> 61

<211> 107

<212> PRT

<213> human

<400> 61

Met	Tyr	Pro	Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val
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Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25					30

Asn	Met	Lys	Lys	Glu	Gln	Asn	Lys	Cys	Phe	Thr	Thr	Pro	Asp	Ser
				35					40					45

Arg	Met	Val	Phe	Ile	Ile	Phe	Ile	Gln	Gln	Arg	Gly	Leu	Asp	Ser
				50					55					60

Lys	Ser	Leu	Gln	Glu	Ile	Asn	Leu	Tyr	Phe	Cys	Glu	Gly	Phe	Tyr
				65					70					75

Thr	Ser	Met	Gln	Leu	Tyr	Lys	Lys	Val	Ile	Arg	Lys	Leu	His	Lys
				80					85					90

Ile	Thr	Gln	Trp	Thr	Arg	Thr	Pro	Gln	Asn	Gln	Ser	Glu	Val	Glu
				95					100					105

Ile Ala